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/feature="exon 13 deletion; first splice variant"
BASE COUNT 462 a 798 c 646 g 328 t

Alignment Scores:
Pred. No.: 0 Length: 2234
Percent Similarity: 1297.50 Matches: 258
Best Local Similarity: 72.62% Conservative: 47
Query Match: 54.43% Mismatches: 84
DB: 1 Indels: 31
Gaps: 9

us-09-670-568b-1 (1-448) x HSY11416 (1-2234)

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DB 159 CACCTCTGGAGCTCTCTGGAACA-----GACAGCACTTAC 194
OY 38 ValAspGluProSerGluAspGlyAlaThrAsnLysIle-----GluIleSer 53
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OY 54 MetAspCysIleLeuMetGlnAspSerAspLeuSerAspProMetIleProGlnIleThr 73
DB 255 ATGACAGCTTCCACCTGAGGAGCATGATCATCT-----GTCAATGGCC 299
OY 74 AsnLeuGlyLeuAsnSerMetAspGlnIleGlnAsnGlySerSerThrSer 93
DB 300 CAGTTCAATCTGCTGAGAGACACCATGACAGATGACAGACCGCGGCTCGGCCAGC 359
OY 94 ProTyrAsnThrAspHisAlaGlnAsnSerValThrAlaProSerProTyrAlaGlnPro 113
DB 360 CCTTACACCCAGAGAGAGCGCCG---AGCGTGCCACCCACTGCGCTTACGCAACCC 416
OY 114 SerSerThrPheAspAlaLeuSerProSerProAlaIleProSerAsnThrAspTyrPro 133
DB 417 AGCTTCACCTTGGACACCATGCGCGGCGCTGTCATCCCTTCACACCGACTTACCC 476
OY 134 GlyProHisSerPheAspValSerPheGlnIleSerSerThrAlaLysSerAlaThrTrp 153
DB 477 GGACCCCACTTGGAGGTACTTTCACAGCATCCACAGCGCCAACTGACCACTGG 536
OY 154 ThrTyrSerThrGluLeuLysLeuTyrCysGlnIleAlaLysThrCysProIleGln 173
DB 537 ACGTACTCCCGCTTGAAGAACTTACTGCGCATGCGCAAGACATGCCCATTCAG 596
OY 174 IleLysValMetThrProProGlnGlnValAlaIleArgAlaMetProValTyrLys 193
DB 597 ATCAAGGTGTCCACCCCGCCACCGCCAGCACTGCCATCCGATCCCTGTTTACAG 656
OY 194 LysAlaGluHisValThrGluValAlaLysArgCysProAsnHisGluLeuSerArgLys 213
DB 657 AAAGCGGAGCAAGTACGAGGTGCTGAAGCGCTGCCCAACACAGAGCTCGGGAGGAC 716
OY 214 PheAsnGluGlyGlnIleAlaProProSerHisLeuIleArgValGluGlyAsnSerHis 233

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DB 777 TCCCACTATGATGATACCTGCTGACCGGACAGCAAGGTGTGTGTGCTTATAGCCA 836
OY 254 ProGlnValGlyThrGluPheThrValLeuTyrAsnPheMetCysAsnSerCys 273
DB 837 CCACAGGTGGGAGCGAATTCACCACTACCTCTTACATCTGTAACAGCACTGT 896
OY 274 ValGlyLysMetAsnArgArgProIleLeuIleValThrLeuGlnThrArgAspGly 293
DB 897 GTAGGGGACATGAACCGCGGCCCATCTCATCATCATCATCATCATCATCATCATCAT 956
OY 294 GlnValLeuGlyArgArgCysPheGluAlaArgIleCysAlaCysProGlnArgAspArg 313
DB 957 CAGTCTGTGGCGCGCGGCTCTTGAAGGCGCGCATCTGTGCGCTGTGCGCGGATGCG 1016
OY 314 LysAlaAspGluAspSerIleArgLysGlnGlnVal-----SerAspSerThrLysAsn 331
DB 1017 AAAGCTGATAGAGACCATACCGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
OY 332 GlyAspGlyThrLysArgProPheArgGlnAsnThrHisGlyIleGlnMet-----Thr 349
DB 1077 GGGGCGCGCCAGCAAGGCTGCTTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
OY 350 SerIleLysArgArgSerProAspAspGluLeuLeuTyrLeuProValArgLysArg 369
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DB 1197 GAGAACTTGTAGATCGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1256
OY 390 GlnHisThrIleGlnThrTyrArgGlnGlnGln-----GlnGlnHisGlnIleLeu 407
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Search completed: July 7, 2003, 08:19:33  
Job time : 3 secs



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	Alignment Scores:				
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us-09-670-568b-1 (1-448) x HSY11416 (1-2234)					
Oy	1	MetserGlnSerThrGlnThrAsnGluPheLeuSerProGlu-----ValPheGln	17		
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Db	159	CACCTCGAGAGCTCTCTGGAACCA-----GACGACACCTAC	194		
Oy	38	ValAspGluProSerGlnAspGlyLarThrAsnLysIle-----GluLeuSer	53		
Db	195	TTTGCACCTTCCCACTGCAACCGGGGGAATTAATGAGTGTGGGCGGAACGATTCCAC	254		
Oy	54	MetaSprCysIleArgMetGlnAspSerAspLeuSerAspMetTyrProGlnTyrThr	73		
Db	255	ATGACAGCTTCCACCTGAGGAGGATGACTATCATCT-----GTCAATGGCC	299		
Oy	74	AsnLeuGlyLeuLeuAsnSerMetAspGlnGlnIleGlnAsnGlySerSerSerThrSer	93		
Db	300	CAGTTCAATCTCTGACGACACACATGACGACAGTAGAGACGCGCGGCTGGCCACG	359		
Oy	94	ProTyrAsnThrAspHisAlaGlnAsnSerValThrAlaProSerProTyrAlaGlnPro	113		
Db	360	CCCTACACCCACAGACGCCGCC---ACCGTGGCCCAACCACTGCCCTACGACACACC	416		
Oy	114	SerSerThrPheAspAlaLeuSerProSerProAlaIleProSerAsnThrAspTyrPro	133		
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Oy	134	GlyProHisSerPheAspValSerPheGlnGlnSerSerThrAlaLysSerAlaThrTyr	153		
Db	477	GAGCCCCACACCTTTAGGTCACTTTCGACGATCCACGACGGCCAAAGTCAAGCCACTGG	536		
Oy	154	ThrTyrSerThrGluLeuLysLysLeuTyrCysGlnIleAlaLysThrCysProIleGln	173		
Db	537	ACGTACTCCCGCTTTGAAGAAACTCTACTGCAATGCGCAAGACATGCCCATTCACAG	596		
Oy	174	IleLysValMetThrProProProGlnGlyAlaValIleLeuGluMetProValTyrLys	193		
Db	597	ATCAAGGTGCCACCCCGCACCCCGACGACTGCCATCCGGGCGCAATGCTGTATACAG	656		
Oy	194	LysAlaGlnHisValThrGluValValLysArgCysProAsnHisGluLeuSerArgGlu	213		
Db	657	AAAGCGACACGCTGACCGACGCTGCGAAACGCTGCCCAACACGAGCTCGGAGAGGAC	716		
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      777  TTCGACATATGTGGATGACCTCTGTACCCGGAGGAGGAGCGCTCGTGTGCCCTATGAGCCA 836
Db      254  ProGlnValGlyThrGluPheThrThrValLeuTyrAsnPhenMetCysAsnSerSerCys 273
      837  CCACAGGTGGGAGCGGAATCACACACATCTCTACAACTTCATGTTGTAACACAGCTGT 896
QY      274  ValGlyClyMetAsnArgArgProIleLeuIleValThrLeuGluThrArgAspGly 293
      897  GTTGGGGGCGATGAAACGGCGGCCCATCTCATCATCATCATCACCCTGGAGATGGCGGATGG 956
Db      294  GlnValLeuGluTyrArgArgCysPheGluValArgIleCysAlaCysProGlyArgAspArg 313
      957  CAGGTGCTGGCGCGCGCTCTTTTGAAGGCGCGCATGCGCCCTGCTCTGCGCGCGACCGA 1016
QY      314  LysAlaAspGluAspSerIleArgGlyGlnGluVal-----SerAspSerThrLysAsn 331
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